

detecting, by computer, changes in connectron behavior in the genome as a function of changes in the sequence of the genome.

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(12)
~~22.~~ A method of modifying, by computer, the expression of different gene collections in a genome, comprising detecting changes in connectron behavior that results in changes in the level of connectron control sequences caused by an exogenous stimulus.

~~23.~~ A method of detecting, by computer, where and when new genes have been integrated into a host genome comprising detecting the operable link between the newly introduced gene and the existing connectron behavior in said host genome.

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~~24.~~ A method of detecting, by computer, the expression effect of different gene collections in a given host genome, comprising detecting the transacting behavior of connectrons between the chromosomes thereof.

~~25.~~ A method of modifying a given genome comprising modifying, by computer, the connectron organization therein.

~~26.~~ A method of detecting, by computer, connectron control and target sequences in a given genome comprising:

determining the base composition of said genome,
determining one or more sites of control sequence
organization, and/or
determining one or more sites of target application.

~~27.~~ A method of determining, by computer, the response of a cell in any tissue to changes in the cell's environment and/or genetic composition comprising providing a complete genomic DNA sequence for the organism and determining the effect of changes in

5 connectrons due to application of a given exogenous stimulus to the genome.

28. Using the method as defined in claim 20, in prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, the tetradic relationship $T1=C1$ and $T2=C2$ where $T1$ and $T2$ are DNA sequences 20 or more bases in length, where the $C1$ sequence is adjacent to the $C2$ sequence, where the $T1$ and $T2$ sequences are on the same chromosome, and where the $C1/C2$ sequences are on the same chromosome as $T1$ and $T2$ or where the $C1/C2$ sequences are on a chromosome different from $T1$ and $T2$, wherein:

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 $C1$ sequence - any positive or negative strand DNA sequence of 20 bases or more, the $C2$ sequence must occur in the same chromosome as the $C1$ sequence,

$C2$ sequence - any positive or negative strand DNA sequence of 20 bases or more, the $C1$ sequence must occur in the same chromosome as the $C2$ sequence,

15 $C1/C2$ - any positive or negative strand DNA sequence of 40 or more bases such that the $C1$ sequence is adjacent to the $C2$ sequence,

20 $T1$ sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the $T2$ sequence, the $T1$ and $T2$ sequences must be between about 1kb and 105kb apart, and

25 $T2$ sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the $T1$ sequence, the $T2$ or $T1$ sequences must be between about 1kb and 105kb apart.

29. Using the method as defined in claim 20, in prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits many different C1/C2 short loops to control the existence of a T1-T2 long loop and wherein
5 said C1/C2 short loops can be on the same chromosome or on different chromosomes from the T1-T2 long loop, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

10 C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

15 C1/C2 - any positive or negative strand DNA sequence of 540 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

20 T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

30. Using the method as defined in claim 20, in prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of many T1-T2 long loops, the C1/C2 short

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5 loop can be on the same chromosome or on different chromosomes from the T1-T2 long loops, wherein:

10 C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

15 C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

20 T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

31. Using the method as defined in claim 20, the connectron relationships between prokaryotes and their plasmids wherein said connectrons implement a control mechanism between the two genomes that makes it possible from them to form a symbiotic relationship, and in the case of D. radiodurans the relationship is not symmetric, and the D. radiodurans genome sends C1/C2 short loops to the MP1 plasmid, wherein:

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C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

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C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

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T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

32. Using the method as defined in claim 20, the connectron relationships that exist in plant or higher animals.

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33. Using the method as defined in claim 20, in prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of one or more T1-T2 long loops without being subject to any expression controls other than those of the gene to which the C1/C2 is 3'UTR, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

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C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

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C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart,

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T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart, and

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3'UTR - untranslated 3' end of an mRNA is beyond the end of the last exon, a stop codon in the mRNA causes the ribosome to stop the translation of mRNA into protein.

34. Using the method as defined in claim 20, in prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of one or more T1-T2 long loops such that this C1/C2 short loop is itself subject to expression control by another T1-T2 long loop which surrounds it, wherein:

5

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

10 C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

15 C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

20 T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

35. Using the method as defined in claim 20, in prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, the connectron relationship that permits one C1/C2 short loop to control the existence of the T1-T2 long loop that surrounds it, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

10 C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 50 or more bases such that the C1 sequence is adjacent to the C2 sequence,

15 T1 sequence - any positive or negative strand DNA sequence of 20bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

20 T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

36. Using the method as defined in claim 20, the connectron relationship that do not have any genes within the T1-T2 long loop, wherein:

5 T1 sequence is any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, and

10 T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, and the T2 or T1 sequences must be between about 1kb and 105kb apart.

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37. Using the method as defined in claim 20, the geneless connectron relationship where one C1/C2 short loop controls the existence of many geneless T1-T2 long loops, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

R E M A R K S

Claims 1 - 19 have been cancelled. Newly added claims 20 - 37 remain in the application.

This will acknowledge the interview courteously granted by Examiner Brusca to applicant's undersigned attorney and the applicant on October 28, 2002. The applicant gave a brief oral description of his connectron technology. A discussion was had of